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RAW SEQUENCE LISTING

DATE: 02/19/2003

PATENT APPLICATION: US/09/982,616

TIME: 14:37:11

Input Set : A:\09982616sequencelisting.txt

Output Set: N:\CRF4\02192003\I982616.raw

4 <110> APPLICANT: Frances E. Lund
 5 Troy D. Randall
 6 Santiago Partida-Sanchez
 8 <120> TITLE OF INVENTION: CD38 MODULATED CHEMOTAXIS
 11 <130> FILE REFERENCE: AP33438 068443.0106
 13 <140> CURRENT APPLICATION NUMBER: 09/982,616
 14 <141> CURRENT FILING DATE: 2001-10-17
 16 <150> PRIOR APPLICATION NUMBER: 60/241,065
 17 <151> PRIOR FILING DATE: 2000-10-17
 19 <160> NUMBER OF SEQ ID NOS: 15
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 1073
 25 <212> TYPE: DNA

ENTERED

26 <213> ORGANISM: Shistosoma mansoni
 28 <400> SEQUENCE: 1
 29 ggaaagaacg tagacatata ttgttatata gatttggttca gttatttttc acaatctttt 60
 30 aattcaaata atgatgaacg taatattgtt tcttacttta tcaaataatt ttgtctttta 120
 31 ctctgcacaa catcaaataa acttacttag tgaaatagta caatcacgat gtactcagtg 180
 32 gaagggttgaa catggagcta ctaatataag ttgtagttag atctggaatt catttgaaaag 240
 33 ctttttactt tcaactcata ctaaactcagc atgtgttatg aaatcagggt tattcgatga 300
 34 ttttgtttat caattgtttg aattggaaca acaacaacaa cagcgacacc acacaattca 360
 35 aacggaacaa tacttccatt ctcaagtgat gaacatcatt cgtggaatgt gtaaactgct 420
 36 tggagtatgt cgttctctag aaactacatt tccaggatat ctgtttgatg aattgaattg 480
 37 gtgtaatggc agtttaacag gcaacacaaa atacgggact gtatgtggat gcgattataa 540
 38 aagtaatgtt gttcatgcgt tctggcaaag tgcttcggct gagtatgcca ggagagcatc 600
 39 tggtaacatc tttgtggtac tgaatggctc ggtcaaagct ccatttaatg aaaataaaac 660
 40 ttttggaata atagaactac cattgttaaa acatcctcga gtacaacaat taacagtga 720
 41 attagttcat agtttggaag atgtaaataa ccgacaaaca tgtgaatcgt ggagtctgca 780
 42 agaacttgca aacaagctga actctgtaca tattcctttt cgttgcattg acgatccttt 840
 43 agagttcaga cattatcaat gcattgaaaa tcctggcaaa caactatgtc agttttcagc 900
 44 ttcgacgagg tcaaactgctg agacattact catacttttt ccgctagtca tttgtttaac 960
 45 tttttatact tccatgaatt gaaataactt ttcagaacta aactttgaac agagaaagag 1020
 46 aacaatgata ataaaggaat aggacattaa tgaaaaaaaa aaaaaaaaaa aaa 1073
 48 <210> SEQ ID NO: 2
 49 <211> LENGTH: 353
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Shistosoma mansoni
 53 <400> SEQUENCE: 2
 54 Glu Arg Thr Thr Tyr Ile Val Ile Ile Cys Ser Val Ile Phe His Asn
 55 1 5 10 15
 56 Leu Leu Ile Gln Ile Met Met Asn Val Ile Leu Phe Leu Thr Leu Ser
 57 20 25 30

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58 Asn Ile Phe Val Phe Asn Ser Ala Gln His Gln Ile Asn Leu Leu Ser
59          35          40          45
60 Glu Ile Val Gln Ser Arg Cys Thr Gln Trp Lys Val Glu His Gly Ala
61          50          55          60
62 Thr Asn Ile Ser Cys Ser Glu Ile Trp Asn Ser Phe Glu Ser Ile Leu
63 65          70          75          80
64 Leu Ser Thr His Thr Lys Ser Ala Cys Val Met Lys Ser Gly Leu Phe
65          85          90          95
66 Asp Asp Phe Val Tyr Gln Leu Phe Glu Leu Glu Gln Gln Gln Gln
67          100          105          110
68 Arg His His Thr Ile Gln Thr Glu Gln Tyr Phe His Ser Gln Val Met
69          115          120          125
70 Asn Ile Ile Arg Gly Met Cys Lys Arg Leu Gly Val Cys Arg Ser Leu
71          130          135          140
72 Glu Thr Thr Phe Pro Gly Tyr Leu Phe Asp Glu Leu Asn Trp Cys Asn
73 145          150          155          160
74 Gly Ser Leu Thr Gly Asn Thr Lys Tyr Gly Thr Val Cys Gly Cys Asp
75          165          170          175
76 Tyr Lys Ser Asn Val Val His Ala Phe Trp Gln Ser Ala Ser Ala Glu
77          180          185          190
78 Tyr Ala Arg Arg Ala Ser Gly Asn Ile Phe Val Val Leu Asn Gly Ser
79          195          200          205
--- -- 80-Val-Lys-Ala-Pro-Phe-Asn-Glu-Asn-Lys-Thr-Phe-Gly-Lys-Ile-Glu-Leu-
81          210          215          220
82 Pro Leu Leu Lys His Pro Arg Val Gln Gln Leu Thr Val Lys Leu Val
83 225          230          235          240
84 His Ser Leu Glu Asp Val Asn Asn Arg Gln Thr Cys Glu Ser Trp Ser
85          245          250          255
86 Leu Gln Glu Leu Ala Asn Lys Leu Asn Ser Val His Ile Pro Phe Arg
87          260          265          270
88 Cys Ile Asp Asp Pro Leu Glu Phe Arg His Tyr Gln Cys Ile Glu Asn
89          275          280          285
90 Pro Gly Lys Gln Leu Cys Gln Phe Ser Ala Ser Thr Arg Ser Asn Val
91          290          295          300
92 Glu Thr Leu Leu Ile Leu Phe Pro Leu Val Ile Cys Leu Thr Phe Tyr
93 305          310          315          320
94 Thr Ser Met Asn Asn Phe Ser Glu Leu Asn Phe Glu Gln Arg Lys
95          325          330          335
96 Arg Thr Met Ile Ile Lys Glu Asp Ile Asn Glu Lys Lys Lys Lys Lys
97          340          345          350
98 Lys
102 <210> SEQ ID NO: 3
103 <211> LENGTH: 1050
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: SM38 consensus sequence
110 <400> SEQUENCE: 3
111 ggaaagaacg tagacatata ttgttatata gatttgttca gttatatttc acaatctttt 60

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112 aattcaaata atgatgaacg taatattgtt tcttacttta tcaaataattt ttgtctttaa 120
113 ctctgcacaa catcaaataa acttacttag tgaaatagta caatcacgat gtactcagtg 180
114 gaaggttgaa catggagcta ctaatataag ttgtagttag atctggaatt catttgaaag 240
115 ctttttactt tcaactcata ctaaatacagc atgtgttatg aaatcagggt tttcgtatga 300
116 ttttgtttat caattgtttg aattggaaca acaacaacaa cagcgacacc acacaattca 360
117 aacggaacaa tacttccatt ctcaagtgat gaacatcatt cgtggaatgt gtaaactgtc 420
118 tggagtatgt cgttctctag aaactacatt tccaggatat ctgtttgatg aattgaattg 480
119 gtgtaatggc agtttaacag gcaacacaaa atacgggact gtatgtggat gcgattataa 540
120 aagtaatggt gttcatgcgt tctggcaaag tgcttcggct gagtatgcca ggagagcatc 600
121 tggtaacatc tttgtggtac tgaatggctc ggtcaaagct ccatttaatg aaaataaaac 660
122 ttttgaaaa atagaactac cattggttaa aacatcctcg agtacaacaa ttaacagtga 720
123 aattagttca tagtttgtaa gatgtaaata accgacaaac atgtgaatcg tggagtctgc 780
124 aagaacttgc aaacaagctg aactctgtac atattccttt tcgttgcatg gacgatcctt 840
125 tagagttcag acattatcaa tgcattgaaa atcctggcaa acaactatgt cagttttcag 900
126 cttcgacgag gtcaaacgtc gagacattac tcatactttt tccgctagtc atttgtttaa 960
127 ctttttatac ttccatgaat tgaataaact tttcagaact aaactttgaa cagagaaaga 1020
128 gaacaatgat aataaaggaa taggmcat 1050
130 <210> SEQ ID NO: 4
131 <211> LENGTH: 473
132 <212> TYPE: DNA
133 <213> ORGANISM: Shistosoma mansoni
135 <400> SEQUENCE: 4
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136 ggctgagtat gccaggagag catctggtaa catctttgtg gtactgaatg gctcgggtcaa 60
137 agctccattt aatgaaaata aaacttttgg aaaaatagaa ctaccattgt taaaacatcc 120
138 tcgagtacaa caattaacag tgaattagt tcatagtttg gaagatgtaa ataaccgaca 180
139 aacatgtgaa tcgtggagtc tgcaagaact tgcaacaag ctgaactctg tacatattcc 240
140 ttttcgttgc attgacgatc ctttagagtt cagacattat caatgcattg aaaatcctgg 300
141 caaacaacta tgtcagtttt cagcttcgac gaggtcaaac gtcgagacat tactcatact 360
142 ttttcgcta gtcatttgtt taacttttta tacttccatg aattgaaata acttttcaga 420
143 actaaacttt gaacagagaa agagaacaat gataataaag gaataggcca tta 473
145 <210> SEQ ID NO: 5
146 <211> LENGTH: 145
147 <212> TYPE: DNA
148 <213> ORGANISM: Shistosoma mansoni
150 <400> SEQUENCE: 5
151 attgaaaatc atggcaaaca actatgtcag ttttcagctt cgacgaggtc aaacgtcgag 60
152 acattactca tactttttcc gctagtcatt tgtttaactt tttatacttc catgaattga 120
153 aataactttt cagaactaaa ctttg 145
155 <210> SEQ ID NO: 6
156 <211> LENGTH: 280
157 <212> TYPE: DNA
158 <213> ORGANISM: Shistosoma mansoni
160 <400> SEQUENCE: 6
161 ggagtatgtc gttctctaga aactacattt ccaggatatc tgtttgatga attgaattgg 60
162 tgcaatggca gtttaacagg caacacaaaa tacgggactg tatgtggatg cgattataaa 120
163 agtaatgttg ttcatgcgtt ctggcaaagt gcttcggctg agtatgccag gagagcatct 180
164 ggtaacatct ttgtggtact gaatggctcg gtcaaagctc catttaatga aaataaaact 240
165 tttggaaaaa tagaactacc attgggttaa acatcctcga 280
167 <210> SEQ ID NO: 7

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168 <211> LENGTH: 1049

169 <212> TYPE: DNA

170 <213> ORGANISM: *Shistosoma mansoni*

172 <400> SEQUENCE: 7

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173 ggaaagaacg tagacatata ttgttatata gatttgttca gttatttttc acaatctttt 60
174 aattcaaata atgatgaacg taatattggt tcttacttta tcaaataattt ttgtctttta 120
175 ctctgcacaa catcaaataa acttacttag tgaaatagta caatcacgat gtactcagt 180
176 gaagggtgaa catggagcta ctaatataag ttgtagttag atctggaatt catttgaaag 240
177 cattttactt tcaactcata ctaaatacagc atgtgttatg aaatcagggt tattcgatga 300
178 ttttgtttat caattgtttg aattggaaca acaacaacaa cagcgacacc acacaattca 360
179 aacggaacaa tacttccatt ctcaagtgat gaacatcatt cgtggaatgt gtaaactgtct 420
180 tggagtatgt cgttctctag aaactacatt tccaggatat ctgtttgatg aattgaattg 480
181 gtgtaatggc agtttaacag gcaacacaaa atacgggact gtatgtggat gcgattataa 540
182 aagtaatggt gttcatgctg tctggcaaa gcttcggct gagtatgcca ggagagcatc 600
183 tggtaacatc tttgtggtac tgaatggctc ggtcaaagct ccatttaatg aaaataaaaac 660
184 ttttggaaaa atagaactac cattgttaaa acatcctcga gtacaacaat taacagtga 720
185 attagttcat agtttgaag atgtaaataa ccgacaaaca tgtgaatcgt ggagtctgca 780
186 agaacttgca aacaagctga actctgtaca tattcctttt cgttgcatg acgatccttt 840
187 agagttcaga cattatcaat gcattgaaaa tcctggcaaa caactatgct agttttcagc 900
188 ttcgacgagg tcaaagctcg agacattact catacttttt ccgctagtca tttgtttaac 960
189 tttttatact tccatgaatt gaaataactt ttcagaacta aactttgaac agagaaagag 1020
190 aacaatgata ataaaggaat aggacatta 1049

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-----192 <210>--SEQ-ID-NO:--8-----

193 <211> LENGTH: 282

194 <212> TYPE: PRT

195 <213> ORGANISM: *Aplysia californica*

197 <400> SEQUENCE: 8

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198 Met Ser Pro Val Ala Ile Val Ala Cys Val Cys Leu Ala Val Thr Leu
199 1 5 10 15
200 Thr Arg Ile Ser Pro Ser Glu Ala Ile Phe Pro Thr Pro Glu Leu Gln
201 20 25 30
202 Asn Val Phe Leu Gly Arg Cys Lys Asp Tyr Glu Ile Thr Arg Tyr Leu
203 35 40 45
204 Thr Ile Leu Pro Arg Val Lys Ser Asp Cys Arg Ala Leu Trp Thr Asn
205 50 55 60
206 Phe Phe Lys Ala Phe Ser Phe Lys Ala Pro Cys Asn Leu Asp Leu Gly
207 65 70 75 80
208 Ser Tyr Lys Asp Phe Phe Gln Arg Ala Gln Gln Thr Leu Pro Lys Asn
209 85 90 95
210 Lys Val Met Phe Trp Ser Gly Val Tyr Asp Glu Ala His Asp Phe Ala
211 100 105 110
212 Asp Asp Gly Arg Lys Tyr Ile Thr Leu Glu Asp Thr Leu Pro Gly Tyr
213 115 120 125
214 Met Leu Asn Ser Leu Val Trp Cys Gly Gln Arg Asp Lys Pro Gly Phe
215 130 135 140
216 Asn Gln Lys Val Cys Pro Asp Phe Lys Asp Cys Pro Val Gln Ala Arg
217 145 150 155 160
218 Glu Ser Phe Trp Gly Thr Ala Ser Ser Ser Tyr Ala His Ser Ala Glu
219 165 170 175

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220 Gly Asp Val Thr Tyr Met Val Asp Gly Ser Asn Pro Lys Val Pro Ala
221      180      185      190
222 Tyr Arg Pro Asp Ser Phe Phe Gly Lys Tyr Glu Leu Pro Asn Leu Thr
223      195      200      205
224 Asn Lys Val Thr Lys Val Lys Val Ile Val Leu His Gln Leu Gly Gln
225      210      215      220
226 Lys Ile Ile Glu Arg Cys Gly Ala Gly Ser Leu Leu Asp Leu Glu Met
227 225      230      235      240
228 Val Val Lys Ala Lys Lys Phe Gly Phe Asp Cys Val Glu Asn Pro Lys
229      245      250      255
230 Ser Val Leu Phe Leu Leu Cys Ala Asp Asn Pro Asn Ala Arg Glu Cys
231      260      265      270
232 Gln Leu Ala Lys Arg Tyr Tyr Arg Ile Ala
233      275      280
236 <210> SEQ ID NO: 9
237 <211> LENGTH: 300
238 <212> TYPE: PRT
239 <213> ORGANISM: Homo sapien
241 <400> SEQUENCE: 9
242 Met Ala Asn Cys Glu Phe Ser Pro Val Ser Gly Asp Lys Pro Cys Cys
243 1      5      10      15
244 Arg Leu Ser Arg Arg Ala Gln Leu Cys Leu Gly Val Ser Ile Leu Val
245 20 25 30
246 Leu Ile Leu Val Val Val Leu Ala Val Val Val Pro Arg Trp Arg Gln
247      35      40      45
248 Gln Trp Ser Gly Pro Gly Thr Thr Lys Arg Phe Pro Glu Thr Val Leu
249      50      55      60
250 Ala Arg Cys Val Lys Tyr Thr Glu Ile His Pro Glu Met Arg His Val
251 65      70      75      80
252 Asp Cys Gln Ser Val Trp Asp Ala Phe Lys Gly Ala Phe Ile Ser Lys
253      85      90      95
254 His Pro Cys Asn Ile Thr Glu Glu Asp Tyr Gln Pro Leu Met Lys Leu
255      100      105      110
256 Gly Thr Gln Thr Val Pro Cys Asn Lys Ile Leu Leu Trp Ser Arg Ile
257      115      120      125
258 Lys Asp Leu Ala His Gln Phe Thr Gln Val Gln Arg Asp Met Phe Thr
259      130      135      140
260 Leu Glu Asp Thr Leu Leu Gly Tyr Leu Ala Asp Asp Leu Thr Trp Cys
261 145      150      155      160
262 Gly Glu Phe Asn Thr Ser Lys Ile Asn Tyr Gln Ser Cys Pro Asp Trp
263      165      170      175
264 Arg Lys Asp Cys Ser Asn Asn Pro Val Ser Val Phe Trp Lys Thr Val
265      180      185      190
266 Ser Arg Arg Phe Ala Glu Ala Ala Cys Asp Val Val His Val Met Leu
267      195      200      205
268 Asn Gly Ser Arg Ser Lys Ile Phe Asp Lys Asn Ser Thr Phe Gly Ser
269      210      215      220
270 Val Glu Val His Asn Leu Gln Pro Glu Lys Val Gln Thr Leu Glu Ala
271 225      230      235      240

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/982,616

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Input Set : A:\09982616sequencelisting.txt

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